

Jarrell, Noble

186188

From: Ramirez, Delia
Sent: Wednesday, April 19, 2006 6:24 PM
To: Jarrell, Noble
Subject: 10/665455

Hi,

I would like to request the following alignments: SEQ ID NO:1 against SEQ ID NO:2-7.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

Noble

ST/Fm 4/23/06

Gen ID 19g

SPR

SUN 7N/A

Go Clear

[Click here to view these alignments graphically with the LALVIEW program \(mime-type *chemical/x-aln2*\).](#)

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)
Sequence 2: UserSeq2, (177 residues)

using the parameters:

SEA ID NO:1 VS SEA ID NO:2
(PROTEIN TRANSLOCATION)

(PROTEIN TRANSLATION)

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.9% identity in 177 residues overlap; Score: 927.0; Gap frequency: 0.0%

```

UserSeq1, 1 MPIEKPEIOHSDFKDLTNLIHFQSMGEKIWLGEORMLLLQ$SAMASFRREMYNTLGIER
UserSeq2, 1 MPIKPKPEIOHSDFKDLTNLIHFQSMGEKIWLGEORMLLLQ$SAMASFRREMYNTLGIER

```

[illegible]

42

UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRG
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRG

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * **

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * **

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL
UserSeq2, 154 GYACAYSSAFMGREI
** * *

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL

[EXPASY Home page](#)
[Site Map](#)
[Search EXPASY](#)
[Contact us](#)
[Swiss-Prot](#)
[Proteomics tools](#)

Search



for



Sim

Click here to view these alignments graphically with the LALNVIEW program ([mime-type chemical/x-aln2](#)).

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4

Seq ID NO:1 VS Seq ID NO:3



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

UserSeq1, 1 MPTAEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTLGIER
UserSeq2, 1 MPIKPKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQFSAMASFRREMTNTLGIER

*** *****

4

42

112

```
UserSeq1,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPT112ELDIDKEYG
UserSeq2,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTGLDIDKEYG
*****
UserSeq1,     121 RFYAEMEWIDWFEEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
UserSeq2,     121 RFYAEMEWIDWFEEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
*****
```

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,      136 ICQTDLG
UserSeq2,      148 VCWTVLG
* * * *
```

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,      148 VCWTVLG
UserSeq2,      136 ICQTDLG
* * * *
```

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      69 GYQSGLKDAELARKL
UserSeq2,     154 GYACAYSSAFMGREI
** * *
```

33.3% identity in 9 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      82 KLRPNASEV
UserSeq2,     107 KVRPTGLDI
```


117

UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDMEYG

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG

36.4% identity in 11 residues overlap; Score: 24.0; Gap frequency: 0.0%

UserSeq1, 82 KLRPNASEVGM
UserSeq2, 107 KVRPTELDIDM
* * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * *

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL
UserSeq2, 154 GYACAYSSAFMGREI

[ExpASY Home page](#)[Site Map](#)[Search ExpASY](#)[Contact us](#)[Swiss-Prot](#)[Proteomics tools](#)

Search



for



Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 936.0; Gap frequency: 0.0%

UserSeq1,
UserSeq2,

1 MPEYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTIGFER
1 MPDKYKPEIQHSDFKDLTNLIHFQSMGKIWLGEQRMILLQSSAMASFRREMTNTIGVER

4

42

58

SEQ ID NO:1 VS SEQ ID NO:5

UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSILKGLVKVRPTELDIDKEYG
UserSeq2, 61 TKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSILKGLVKVRPTELDIDKEYG

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMOPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMOPVCWTVLGYACAYSSAFMGREIIFKEVSCRCGG

140

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * * *

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 69 GYQSGLKDAELARKL
UserSeq2, 154 GYACAYSSAFMGREI
* * * *

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL

clear

[Click here to view these alignments graphically with the LALVIEW program \(mime-type chemical/x-aln2\).](#)

Click here to download LALNVIEW (Unix, Mac and PC versions available).

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

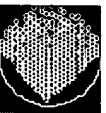
using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

97.2% identity in 180 residues overlap; Score: 932.0; Gap frequency: 0.0%

```

UserSeq1, 1 MPIEKPEIOHSDFKDLTNLIHFQSMEGKIWLGEQRMILLQ$AMASFRREMYNTLGIER
UserSeq2, 1 MPIKPKPEIOHSDFKDLTNLIHFOSMEGKIWLGEORMLLQ$AMASFRREMYNTLGIER

```

1 MPEYKPEI OHSDFKD LTNL IHFQSM EGIWLGEO RMLLLQSSAMASFRE MVNTLGI ER
1 MPEYKPEI OHSDFKD LTNL IHFQSM EGIWLGEO RMLLLQSSAMASFRE MVNTLGI ER
1 MPEYKPEI OHSDFKD LTNL IHFQSM EGIWLGEO RMLLLQSSAMASFRE MVNTLGI ER

5

42

Seed ID M.1 VS Seed ID N0:6

116-117

```
UserSeq1, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
UserSeq2, 61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIGREYG
*****

UserSeq1, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
UserSeq2, 121 RFYAEMEMIDWFEVEICQTDLGQMDDPVCWTVLGYACAYSSALMGREIIFKEVSCRGGCGG
*****

40.0% identity in 10 residues overlap; Score: 26.0; Gap frequency: 0.0%

UserSeq1, 82 KLRPNASEVG
UserSeq2, 107 KVRPTELDIG
* * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 148 VCWTVLG
UserSeq2, 136 ICQTDLG
* * *

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

UserSeq1, 136 ICQTDLG
UserSeq2, 148 VCWTVLG
* * *

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

UserSeq1, 154 GYACAYSSAFMGREI
UserSeq2, 69 GYQSGLKDAELARKL
```

1

Click here to view these alignments graphically with the LALVIEW program (mime-type *chemical/x-aln2*).

[Click here to download LALNVIEW \(Unix, Mac and PC versions available\).](#)

You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: UserSeq1, (180 residues)

Sequence 2: UserSeq2, (180 residues)

Steer ID No: 1 vs Steer ID No: 7

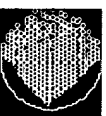
using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 20

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

98.3% identity in 180 residues overlap; Score: 941.0; Gap frequency: 0.0%

1 UserSeq1, 1 MPTEKPEIOHSDFKDLTNLIHFQSMGEKIWLGEQRMILLQSSAMASFRREMYNTLIGIER
1 UserSeq2, 1 MPTEKPEIOHSDFKDLTNLIHFQSMGEKIWLGEQRMILLQSSAMASFRREMYNTLIGIER
1 MPTEKPEIOHSDFKDLTNLIHFQSMGEKIWLGEQRMILLQSSAMASFRREMYNTLIGIER

[illegible]

五

42

```
UserSeq1,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
UserSeq2,      61 AKGLFLRHGYQSGLKDAELARKLRPNASEVGMFLAGPQMHSLKGLVKVRPTELDIDKEYG
*****
```

```
UserSeq1,      121 RFYAEMEMIDWFEVEICQTDLDGQMDDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
UserSeq2,      121 RFYAEMEMIDWFEVEICQTDLPQMDPVCWTVLGYACAYSSAFMGREIIFKEVSCRGGCGG
*****
          141
```

57.1% identity in 7 residues overlap; Score: 22.0; Gap frequency: 0.0%

```
UserSeq1,      136 ICQTDLG
UserSeq2,      148 VCWTVLG
          * * * *
```

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      154 GYACAYSSAFMGREI
UserSeq2,      69 GYQSGLKDAELARKL
          ** * *
```

26.7% identity in 15 residues overlap; Score: 21.0; Gap frequency: 0.0%

```
UserSeq1,      69 GYQSGLKDAELARKL
UserSeq2,      154 GYACAYSSAFMGREI
          ** * *
```

33.3% identity in 9 residues overlap; Score: 20.0; Gap frequency: 0.0%

```
UserSeq1,      107 KVRPTELDI
UserSeq2,      82 KLRPNASEV
```